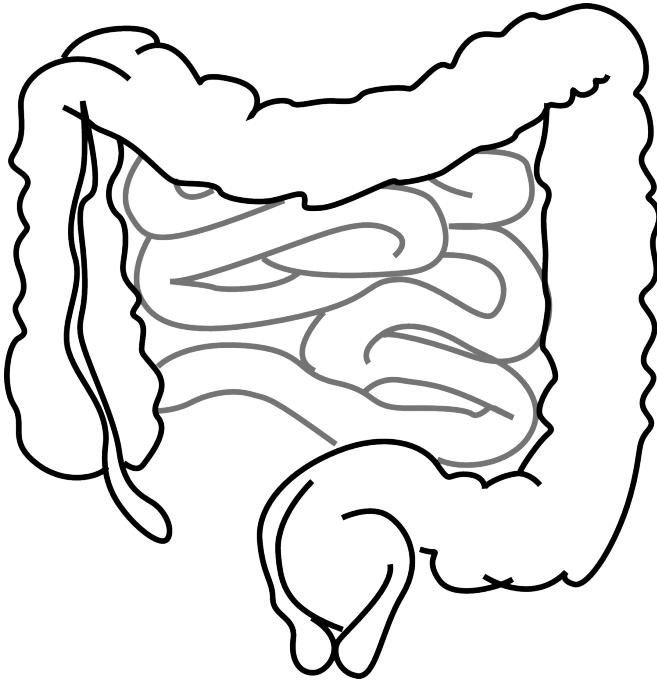


Gut fungi could play a role in obesity epidemic

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Credit: CC0 Public Domain

A high-fat diet changes fungi in the gut and may play a role in the development of obesity, according to a new study in *mSphere*, a journal of the American Society for Microbiology. While gut microbes have previously been implicated in the development of obesity, this study shows that fungi may also play a role.

"We really need to be looking at all the microbes and how they are interacting with each other to get a full picture of what the microbiome structure and function is in a given individual," said principal investigator Cheryl Gale, MD, associate professor in the Department of Pediatrics at the University of Minnesota, in Minneapolis.

In recent years, research has revealed that [gut microbes](#) are involved in the development of

obesity, but characterization of microbiota in lean versus obese individuals has been dominated by studies of [gut bacteria](#), ignoring the potential contributions of fungi on metabolic health. "Fungi have recently been shown to affect [gut inflammation](#)," said Dr. Gale. Although they represent a small component of the microbiota, fungal communities are significant in that they potentially serve as a reservoir for pathogens as well as for keystone species with critical roles in maintaining the function of the gut microbiome. (image: [bacteria](#) in the gut, from NIAID)

In the new study, mice fed a high-fat [diet](#) had significantly different abundances of 19 bacterial and 6 fungal taxa than mice fed a standard diet, with a [high-fat diet](#) causing a similar magnitude of change in overall fungal and bacterial microbiome structures. Predicted microbiome functional modules related to metabolism were significantly less abundant in high-fat diets. The researchers also identified correlations of coabundance between specific fungi and bacteria in mice that are fed a normal diet and found that the number of these coabundance correlations decreased in the mice that were fed high-fat diets.

"Not only are we affecting the community of fungi with dietary change, but we also see that relationships between fungi and bacteria are changing," said Dr. Gale. "These kingdoms are not in isolation. If one changes, it is going to impact the community structure and maybe the functional structure of other kingdoms as well. I think that is where the microbiome field is moving."

The results of the study support the inclusion of fungal community analyses in studies that seek to discover new connections between intestinal microbiomes and [metabolic health](#). Dr. Gale pointed out that sequencing fungi is more challenging than sequencing bacteria. "The methods development hasn't caught up to where it is with bacteria. You need very sensitive methods

because fungi are less abundant," said Dr. Gale.
"We haven't developed the databases of sequences for [fungi](#) like we have for bacteria. The databases aren't as rich, so when you sequence the fungal community, you often get sequences that don't match to anything."

Provided by American Society for Microbiology

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